

GenCore version 5.1.4_P5_4578
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OM protein - protein search, using sw model

Run on: March 24, 2003, 15:45:24 ; Search time 11.0303 seconds

(without alignment)
977.656 Million cell updates/sec

Title: US-09-988-971-2_COPY_2_261

Perfect score: 1346
Sequence: 1 GSLPSRRKSLPSPSLSSVQ.....RESLFSYISLNDVAISLDA 260

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	374.5	27.8	511	LYN_HUMAN	P07948 homo sapien
2	371.5	27.6	511	LYN_MOUSE	P25811 mus musculu
3	371.5	27.6	511	LYN_RAT	Q07014 ratu
4	364.5	27.1	526	HCK_HUMAN	P08631 homo sapien
5	362	26.9	504	HCK_MACFA	Q95M30 macaca fasc
6	356.5	26.5	504	BLK_HUMAN	P51451 homo sapien
7	356	26.4	524	HCK_MOUSE	P08103 mus musculu
8	355.5	26.4	503	HCK_RAT	P50545 ratu
9	345.5	25.7	498	BLK_MOUSE	P16277 mus musculu
10	344	25.6	508	LCK_HUMAN	P06239 homo sapien
11	342.5	25.4	508	LCK_MOUSE	P06240 mus musculu
12	337	25.0	507	LCK_CHICK	P42683 gallu
13	323.5	24.0	537	YES_XENLA	P10936 xenopus lae
14	321	23.8	541	YES_CHICK	P09324 gallu
15	319.5	23.7	536	LYN_HUMAN	P06241 homo sapien
16	319.5	23.7	543	YES_HUMAN	P07947 homo sapien
17	316.5	23.5	529	LYN_HUMAN	P09479 homo sapien
18	315	23.4	544	YES_HIPHE	P27447 xiphophoru
19	314.5	23.4	536	LYN_XENLA	P13406 xenopus lae
20	313	23.3	528	YES_AVISY	P130527 avian sarco
21	313	23.3	533	LYN_MOUSE	P33688 mus musculu
22	309.5	23.0	536	LYN_XIPHE	P27446 xiphophoru
23	309.5	23.0	541	YES_MOUSE	Q04736 mus musculu
24	307	22.8	517	LYN_MOUSE	P14234 mus musculu
25	305	22.7	535	LYN_CHICK	Q02977 gallu
26	304	22.6	539	YES_CANFA	Q28923 canis fami
27	301.5	22.4	533	LYN_CHICK	Q05876 gallu
28	294	21.8	506	SRK4_SPOLA	P42890 spongilla
29	290.5	21.6	526	LYN_XENLA	P00525 avian sarco
30	290.5	21.6	532	LYN_CHICK	P00523 gallu
31	290.5	21.6	552	LYN_CHICK	P00528 drosophila
32	290.5	21.6	557	LYN_CHICK	P14085 avian sarco
33	290.5	21.6	587	LYN_CHICK	P15054 avian sarco

34	288.5	21.4	568	1	SRC_AVISY	P14084 avian sarco
35	281.5	20.9	535	1	SRC_RAT	Q9W493 ratu
36	280.5	20.8	526	1	SRC_REVSER	P00524 rous sarcom
37	280.5	20.8	535	1	SRC_HUMAN	P12931 homo sapien
38	280	20.7	509	1	STK_HYDAT	P17713 hydat alien
39	278.5	20.7	531	1	SRG2_XENLA	P13116 xenopus lae
40	277.5	20.6	526	1	SRC_FGVP	P00526 rous sarcom
41	275.5	20.5	540	1	SRC_MOUSE	P05480 mus musculu
42	273.5	20.3	531	1	SRC2_XENLA	P13115 xenopus lae
43	272.5	20.2	526	1	SRC_RESVH	P25020 rous sarcom
44	271	20.1	505	1	SRK1_SPOLA	P42686 spongilla
45	261	19.4	545	1	LYN_FGVP	P00544 feline sarco

ALIGNMENTS

```

RESULT 1
LYN_HUMAN
ID LYN_HUMAN STANDARD; PRT; 511 AA.
AC P07948;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tyrosine-protein kinase LYN (EC 2.7.1.112).
GN LYN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP MEDLINE=9712710; PubMed=3561390;
RA Yamashita Y., Fukushige S.-I., Semba K., Sukegawa J., Miyajima N.,
RA Matsubara K.-I., Yamamoto T., Toyoshima K.;
RT "The yes-related cellular gene lyn encodes a possible tyrosine kinase
RT similar to p56lck."
RT Mol. Cell. Biol. 7:237-243(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94171041; PubMed=8125304;
RA Rider L.G., Raben N., Miller L., Jelasma C.;
RT "The CDNA encoding two forms of the LYN protein tyrosine kinase are
RT expressed in rat mast cells and human myeloid cells."
RL Gene 138:219-222(1994).
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS, LYN A (SHOWN HERE) AND LYN B;
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
CC SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
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DR EMBL: M16038; AA59540.1; -
DR EMBL: M79321; AA55019.1; -
DR PIR: A26719; TYRHLY.
DR HSSP: P08631; IADS.
DR GENE: 165120; -
DR MIM: 165120; -
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR000980; SH2.
DR InterPro: IPR001452; SH3.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00017; SH2; 1.

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DR Pfam; PF00018; SH3; 1.
 DR Pfam; PF00069; kinase; 1.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR PRODOM; PD000001; Euk_kinase; 1.
 DR PRODOM; PD000066; SH3; 1.
 DR PRODOM; PD000093; SH2; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00219; TYRC; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KW Proto-oncogene; Tyrosine-protein kinase; Phosphorylation;
 KW Transferase; ATP-binding; Myristate; SH2 domain; SH3 domain;
 KW Palmitate; Lipoprotein; Alternative splicing.
 FT INIT MET 0
 FT LIPID 1 1 MYRISTATE (BY SIMILARITY).
 FT LIPID 2 2 PALMITATE (BY SIMILARITY).
 FT DOMAIN 62 122 SH3.
 FT DOMAIN 128 225 SH2.
 FT NP_BIND 246 500 PROTEIN_KINASE.
 FT BINDING 252 260 ATP (BY SIMILARITY).
 FT ACT_SITE 274 274 ATP (BY SIMILARITY).
 FT MOD_RES 366 366 BY SIMILARITY.
 FT MOD_RES 396 396 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD_RES 507 507 PHOSPHORYLATION (BY SIMILARITY).
 FT VAR_SEQ 42 42 MISSING (IN ISOFORM LYN B).
 SO SEQUENCE 511 AA; 58442 MW; 8419CD461204E364 CRC64.

Query Match 27.8%; Score 374.5; DB 1; Length 511;
 Best Local Similarity 40.3%; Pred. No. 2,7e-24;
 Matches 81; Conservative 36; Mismatches 75; Indels 9; Gaps 3;

OY 5 SRKSLPSPLSSSVGGVTVAEARSKATVALGSPGAPAEISRLSEPTLYSED 64
 DB 37 SNKQGRVPE-SQLLPGQRCTDPPEQDLYVALYDHIHDDLSFKGEKKVLEEH 95
 OY 65 GDMWTVLSEVSGREYNIPSVHAKV---SHGWLVEGLSEKAEILLPGNPGGATLIR 120
 DB 96 GEMWKAASLITKEGFIIPSNVAKLNTLETETWEPFKITKDBROLAPNSAGAEILR 155
 OY 121 ESOTRRGYSLSVRLSPRPAWDRIHRYRHICLDNWMYIYSPRLTFFSLCALVDYSLAD 180
 DB 156 ESETLKGSTLSVDRPDVPHVNDYIKYKIRSLDNGCYIISPRITFCISDMIKYKQKD 215
 OY 181 DICCLKEPCVLQRAAPLPGR 201
 DB 216 GLCRLEKACI---SPKPOK 232

RESULT 2

LYN_MOUSE

STANDARD;

PRT; 511 AA.

AC P25911; O62127; 22, Created)
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase LYN (EC 2.7.1.112).
 GN LYN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91260688; PubMed=1710766;
 RA Stanley E., Ralph S.J., McEwen S., Boulet I., Holtzman D.A.,
 RA Lock P., Dunn A.R.;
 RT "Alternatively spliced murine lyn mRNAs encode distinct proteins";
 RL Mol. Cell. Biol. 11:3399-3406 (1991).

RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91203857; PubMed=2017160;
 RA Yi T., Bojlen J.B., Ihle J.N.;
 RT "Hematopoietic cells express two forms of lyn kinase differing by 21
 RT amino acids in the amino terminus";
 RL Mol. Cell. Biol. 11:2391-2396 (1991).
 RN [3]
 RP SEQUENCE OF 363-431 FROM N.A.
 RX MEDLINE=90152381; PubMed=2482828;
 RA Wilks A.F., Kudan R.R., Hovens C.M., Ralph S.J.;
 RT "The application of the polymerase chain reaction to cloning members
 RT of the protein tyrosine kinase family";
 RL Gene 85:67-74 (1989).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; LYN A (SHOWN HERE) AND LYN B;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN B-LYMPHOID AND
 CC MYELOID CELLS.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
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 CC -----
 DR EMBL; M64608; AAA39470.1; -;
 DR EMBL; M57696; AAA39471.1; -;
 DR EMBL; M57697; AAA39472.1; -;
 DR EMBL; M33426; AAA40017.1; -;
 DR PIR; A39719; A39719.
 DR HSSP; P08631; IAD5.
 DR MGI; MGI:96892; LYN.
 DR InterPro; IPR000719; Euk_kinase.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR Pfam; PF00069; kinase; 1.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR PRODOM; PD000001; Euk_kinase; 1.
 DR PRODOM; PD000066; SH3; 1.
 DR PRODOM; PD000093; SH2; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00219; TYRC; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KW Proto-oncogene; Tyrosine-protein kinase; Phosphorylation;
 KW Transferase; ATP-binding; Myristate; SH2 domain; SH3 domain;
 KW Palmitate; Lipoprotein; Alternative splicing.
 FT INIT MET 0
 FT LIPID 1 1 MYRISTATE (BY SIMILARITY).
 FT LIPID 2 2 PALMITATE (BY SIMILARITY).
 FT DOMAIN 62 122 SH3.
 FT DOMAIN 128 225 SH2.
 FT NP_BIND 246 500 PROTEIN_KINASE.
 FT BINDING 252 260 ATP (BY SIMILARITY).
 FT BINDING 274 274 ATP (BY SIMILARITY).
 FT ACT_SITE 366 366 BY SIMILARITY.
 FT MOD_RES 396 396 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

FT MOD_RES 507 507 PHOSPHORYLATION (BY SIMILARITY).
 FT VASBPIC 24 44 MISSING (IN ISOFORM LYN B).
 FT CONFLICT 76 76 I -> F (IN REF. 2).
 FT CONFLICT 160 160 L -> I (IN REF. 2).
 FT CONFLICT 278 278 P -> L (IN REF. 2).
 FT CONFLICT 390 390 V -> I (IN REF. 2).
 FT CONFLICT 414 414 I -> F (IN REF. 3).
 FT CONFLICT 424 424 D -> N (IN REF. 1).
 FT CONFLICT 431 431 L -> P (IN REF. 3).
 SQ SEQUENCE 511 AA; 58681 MW; 3935221CC90C50F0 CRC64;
 Query Match 27.6%; Score 371.5; DB 1; Length 511;
 Best Local Similarity 40.8%; Pred. No. 4,9e-24;
 Matches 82; Conservative 33; Mismatches 77; Indels 9; Gaps 3;
 QY 5 SRRKSLPSLSSVOCQPVYMEARSKATAYAGSPAGAPALSLRGEPLTIVSED 64
 DB 37 SNKQORVPER-HLFGQRFQTKPEEGQIVVALPYDGHFDLSFKGKMKVLEEH 95
 QY 65 GDMWTVLSEVSGREYINIPSVHAKV---SHGWLVEGLSRKAEELLLPGNPGAFILR 120
 DB 96 GEMWKAISLSKREGFIPSNVYAKVNTLETETEFKDIIRKDAERQLAFAVNSAGAFILR 155
 QY 121 ESQTRGYSVLSVLRSPASMDRIHYRIHCLDNGWLYTISPLTFPEPLQALVDHYSELD 180
 DB 156 ESETLKGSFSLVRDYPDHGHVAKHKIKSLDNGYIISRIITFPCISDMIKHYOKSD 215
 QY 181 DICLLKEPCVLOKAGPLDGK 201
 DB 216 GLCRRLERAKCI---SPKPK 232
 RESULT 3
 LYN_RAT STANDARD; PRT; 511 AA.
 ID LYN_RAT
 AC Q07014; Q63320; Created
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase LYN (EC 2.7.1.12).
 GN LYN.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Euteleostomi; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Minoguchi K., Nishikata H., Siraganian R.P.;
 RT "Bacterially expressed rat p56lyn binds several proteins in rat
 RT basophilic leukemia cells including pp72, a tyrosine phosphorylated
 RT protein prominent in activated cells.";
 RL J. Immunol. 150:222-222(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=94171041; PubMed=8125304;
 RA Rider L.G., Raben N., Miller L., Jelsema C.;
 RT "The cdna encoding two forms of the lyn protein tyrosine kinase are
 RT expressed in rat mast cells and human myeloid cells.";
 RL Gene 138:219-222(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=97442484; PubMed=9295361;
 RA Vonakis B.M., Chen H., Haleem-Smith H., Metzger H.;
 RT "The unique domain as the site on lyn kinase for its constitutive
 RT association with the high affinity receptor for Ige.";
 RL J. Biol. Chem. 272:24072-24080(1997).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS, LYN A (SHOWN HERE) AND LYN B;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN B-LYMPHOID AND
 CC MYELOID CELLS.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC

CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
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 CC -----
 DR EMBL; L14951; AAA1549.1; -;
 DR EMBL; L14782; AAA20945.1; -;
 DR EMBL; L14823; AAA20945.1; -;
 DR EMBL; AF000300; AAB71344.1; -;
 DR EMBL; AF000301; AAB71345.1; -;
 DR EMBL; AF000302; AAB71346.1; -;
 DR HSSP; P08631; 1AD5.
 DR Interpro; IPR000719; Euk_pkinase.
 DR Interpro; IPR000980; SH2.
 DR Interpro; IPR001452; SH3.
 DR Interpro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR ProDom; PD000066; SH3; 1.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00219; Tyrc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KW Proto-oncogene; Tyrosine-protein kinase; Phosphorylation;
 KW Transferase; ATP-binding; Myristate; SH2 domain; SH3 domain;
 KW Palmitate; Lipoprotein; Alternative splicing.
 KW INT_MET 0
 FT LIPID 1 1
 FT LIPID 2 2
 FT DOMAIN 62 122
 FT DOMAIN 128 225
 FT NP_BIND 246 500
 FT BINDING 252 260
 FT BINDING 274 274
 FT ACT_SITE 366 366
 FT MOD_RES 396 396
 FT MOD_RES 507 507
 FT VASBPIC 24 44
 FT CONFLICT 230 230
 FT CONFLICT 307 307
 FT CONFLICT 418 418
 SQ SEQUENCE 511 AA; 58529 MW; 24425E229CD43ED CRC64;
 Query Match 27.6%; Score 371.5; DB 1; Length 511;
 Best Local Similarity 40.8%; Pred. No. 4,9e-24;
 Matches 82; Conservative 33; Mismatches 77; Indels 9; Gaps 3;
 QY 5 SRRKSLPSLSSVOCQPVYMEARSKATAYAGSPAGAPALSLRGEPLTIVSED 64
 DB 37 SNKQORVPER-HLFGQRFQTKPEEGQIVVALPYDGHFDLSFKGKMKVLEEH 95
 QY 65 GDMWTVLSEVSGREYINIPSVHAKV---SHGWLVEGLSRKAEELLLPGNPGAFILR 120
 DB 96 GEMWKAISLSKREGFIPSNVYAKVNTLETETEFKDIIRKDAERQLAFAVNSAGAFILR 155
 QY 121 ESQTRGYSVLSVLRSPASMDRIHYRIHCLDNGWLYTISPLTFPEPLQALVDHYSELD 180

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 DR EMBL, M16591; AAA52643.1; -
 DR EMBL, M16592; AAA52644.1; -
 DR EMBL, BC014435; AAH14435.1; -
 DR EMBL, AK026432; BAB15482.1; -
 DR EMBL, AL049539; CAB75606.1; -
 DR EMBL, X58741; CAA1565.2; -
 DR EMBL, X58742; CAA1565.2; JOINED.
 DR EMBL, X58743; CAA1565.2; JOINED.
 DR PIR, A27812; TVHUC.
 DR PDB, 2HCK; 20-AUG-97.
 DR PDB, 3HCK; 15-OCT-97.
 DR PDB, 4HCK; 17-JUN-98.
 DR PDB, 5HCK; 17-JUN-98.
 DR PDB, 1AD5; 15-MAY-97.
 DR PDB, 1BUI; 11-NOV-98.
 DR Genew; HGNC:4840; HCK.
 DR MIM, 142370; -
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR000980; SH3.
 DR InterPro; IPR001452; SH3.
 DR InterPro; IPR002290; Sec_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 2.
 DR Pfam; PF00069; pkinase; 4.
 DR ProDom; PD000066; SH3; 1.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00219; TYKc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 DR Transferase; Tyrosine-protein kinase; phosphorylation; ATP-binding;
 DR Myristate; SH2 domain; SH3 domain; Alternative initiation;
 DR 3D-structure.
 FT CHAIN 1 526
 FT INIT MET 22 526 TYROSINE-PROTEIN KINASE P59-HCK.
 FT DOMAIN 78 138 FOR ISOFORM P59-HCK.
 FT DOMAIN 144 241 SH2.
 FT NP BIND 266 276 PROTEIN KINASE.
 FT BINDING 290 290 ATP.
 FT ACT_SITE 381 381
 FT LIPID 2
 FT LIPID 23 MYRISTATE (BY SIMILARITY).
 FT MOD_RES 411 411 C -> S (IN REF. 1).
 FT CONFLICT 24 24 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT CONFLICT 144 144 W -> R (IN REF. 4).
 SO SEQUENCE 526 AA; 59599 MW; 847B877A0A641725 CRC64;

Query Match 27.18; Score 364.5; DB 1; Length 526;
 Best Local Similarity 42.28; Pred. No. 2e-23;
 Matches 78; Conservative 31; Mismatches 69; Indels 7; Gaps 2;

QY 11 PPSPLSSVQGGPVTMEAEBSKATAVAGSPAGPAEELSLRGEELTVSEDDGMMTV 70
 DB 61 PGRNSHNS---NTFGIRAGSEDIYVALYDEALHEDLSFGQGMVTVLEESGEWKA 117
 QY 71 LSEVSGRETNISGVAVAVY---SHGWLVEGLSRKAEELLLLPGNGGAFLLIRSQTRR 126
 DB 118 RSLATREGTIPSNVYARVDLFTTEEFKGISRDARERQLALPGMLGSPFMRDSEYTK 177

QY 127 GSYSLSVRLSPASMDRIHRYRHCIDNGMLYSRLTFPSLQALVDHYSELADICCL 186
 DB 178 GSYSLSVRLSPASMDRIHRYRHCIDNGMLYSRLTFPSLQALVDHYSELADICCL 237
 QY 187 KEPCV 191
 DB 238 SVPCW 242

RESULT 5

HCK_MACFA STANDARD; PRT; 504 AA.

AC 095630;
 DT 15-JUN-2002 (rel. 41, Created)
 DT 15-JUN-2002 (rel. 41, Last sequence update)
 DT 15-JUN-2002 (rel. 41, Last annotation update)
 DE Tyrosine-protein kinase HCK (EC 2.7.1.112) (p56-HCK) (Hemopoietic cell
 DE kinase).
 GN HCK.

OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 NCBI_TaxID=9541;

RA Picard C.;
 RP SEQUENCE FROM N.A.

RL Thesis (2001), University of Marseille, France.

CC -!- FUNCTION: MAY SERVE AS PART OF A SIGNALING PATHWAY COUPLING THE FC
 CC RECEPTOR TO THE ACTIVATION OF THE RESPIRATORY BURST. MAY ALSO
 CC CONTRIBUTE TO NEUTROPHIL MIGRATION AND MAY REGULATE THE
 CC DEGRANULATION PROCESS OF NEUTROPHILS (By similarity).

CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -!- SUBCELLULAR LOCATION: Membrane-associated (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUBFAMILY.

CC -!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.

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 CC or send an email to license@isb-sib.ch).

CC EMBL, AJ320181; CAC44031.1; -
 CC InterPro; IPR000719; Euk_pkinase.
 CC InterPro; IPR000980; SH2.
 CC InterPro; IPR001452; SH3.
 CC InterPro; IPR001245; Tyr_pkinase.
 CC Pfam; PF00017; SH2; 1.
 CC Pfam; PF00018; SH3; 1.
 CC Pfam; PF00069; pkinase; 4.
 CC ProDom; PD000066; SH3; 1.
 CC ProDom; PD000093; SH2; 1.
 CC PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 CC PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
 CC PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 CC PROSITE; PS50001; SH2; 1.
 CC PROSITE; PS50002; SH3; 1.

DR Transferase; Tyrosine-protein kinase; phosphorylation; ATP-binding;
 DR Myristate; SH2 domain; SH3 domain.
 DR 3D-structure.
 FT CHAIN 1 526
 FT INIT MET 22 526 TYROSINE-PROTEIN KINASE P59-HCK.
 FT DOMAIN 78 138 FOR ISOFORM P59-HCK.
 FT DOMAIN 144 241 SH2.
 FT NP BIND 266 276 PROTEIN KINASE.
 FT BINDING 290 290 ATP.
 FT ACT_SITE 381 381
 FT LIPID 2
 FT LIPID 23 MYRISTATE (BY SIMILARITY).
 FT MOD_RES 411 411 C -> S (IN REF. 1).
 FT CONFLICT 24 24 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT CONFLICT 144 144 W -> R (IN REF. 4).
 SO SEQUENCE 526 AA; 59599 MW; 847B877A0A641725 CRC64;

Query Match 27.18; Score 364.5; DB 1; Length 526;
 Best Local Similarity 42.28; Pred. No. 2e-23;
 Matches 78; Conservative 31; Mismatches 69; Indels 7; Gaps 2;

QY 11 PPSPLSSVQGGPVTMEAEBSKATAVAGSPAGPAEELSLRGEELTVSEDDGMMTV 70
 DB 61 PGRNSHNS---NTFGIRAGSEDIYVALYDEALHEDLSFGQGMVTVLEESGEWKA 117
 QY 71 LSEVSGRETNISGVAVAVY---SHGWLVEGLSRKAEELLLLPGNGGAFLLIRSQTRR 126
 DB 118 RSLATREGTIPSNVYARVDLFTTEEFKGISRDARERQLALPGMLGSPFMRDSEYTK 177

RP SEQUENCE OF 22-524 FROM N.A.
 RX MEDLINE=8068567; PubMed=3317404;
 RA Holzman D.A., Cook W.D., Dunn A.R.;
 RT "Isolation and sequence of a cDNA corresponding to a src-related gene
 RT expressed in murine hemopoietic cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:8325-8329(1987).
 RN [3]
 RP SEQUENCE OF 1-22 FROM N.A., AND ALTERNATIVE INITIATION.
 RX MEDLINE=91342636; PubMed=1875927;
 RA Lock P., Ralph S., Stanley E., Boulet I., Ramsay R., Dunn A.R.;
 RT "Two isoforms of murine hck, generated by utilization of alternative
 RT translational initiation codons, exhibit different patterns of
 RT subcellular localization.";
 RL Mol. Cell. Biol. 11:4363-4370(1991).
 CC -1- FUNCTION: MAY SERVE AS PART OF A SIGNALING PATHWAY COUPLING THE FC
 CC RECEPTOR TO THE ACTIVATION OF THE RESPIRATORY BURST. MAY ALSO
 CC CONTRIBUTE TO NEUTROPHIL MIGRATION AND MAY REGULATE THE
 CC DEGRANULATION PROCESS OF NEUTROPHILS.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: P59-HCK AND P56-HCK ARE ASSOCIATED WITH
 CC MEMBRANES. P59-HCK IS ALSO CYTOPLASMIC.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1P59-HCK (shown here) and P56-
 CC HCK; are produced by alternative initiation.
 CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN CELLS OF THE
 CC MYELOID AND B-LYMPHOID LINEAGES.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: Y00487; CAA68544.1; -;
 DR EMBL: J03023; AAA37305.1; -;
 DR PIR: A27282; TYMSHC
 DR PIR: A39973; A39973.
 DR HSSP: P08631; IAD5.
 DR MGD: MG1:96052; HCK.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 1.
 DR Pfam: PF00069; pkinase; 1.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR ProDom: PD000066; SH3; 1.
 DR ProDom: PD000093; SH2; 1.
 DR SMART: SM00252; SH2; 1.
 DR SMART: SM00326; SH3; 1.
 DR SMART: SM00219; Tyrc; 1.
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE: PS00109; PROTEIN KINASE TYR; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS50001; SH2; 1.
 DR PROSITE: PS50002; SH3; 1.
 DR Transferase: Tyrosine-protein kinase; phosphorylation; ATP-binding;
 KW Myristate; SH2 domain; SH3 domain; Alternative initiation;
 KW CHAIN 1 524
 FT CHAIN 1 524 TYROSINE-PROTEIN KINASE P59-HCK.
 FT INT_MET 22 524 TYROSINE-PROTEIN KINASE P56-HCK.
 FT DOMAIN 76 136 FOR ISOFORM P56-HCK.
 FT DOMAIN 142 239 SH2.

FT DOMAIN 260 513 PROTEIN KINASE.
 FT NP_BIND 266 274 ATP (BY SIMILARITY).
 FT BINDING 288 288 ATP (BY SIMILARITY).
 FT ACT_SITE 379 379 BY SIMILARITY.
 FT LIPID 2 2 MYRISTATE (BY SIMILARITY).
 FT LIPID 23 23 MYRISTATE (BY SIMILARITY).
 FT MOD_RES 409 409 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 SQ SEQUENCE 524 AA; 59129 MW; DF72FD693809706 CRC64;
 Query Match 26.4%; Score 356; DB 1; Length 524;
 Best Local Similarity 41.5%; Pred. NO. 1e-22;
 Matches 83; Conservative 33; Mismatches 72; Indels 12; Gaps 4;
 QY 10 LPPSSSSVQCGGVWTE---AERKAT-AVALGSFPAGAPNELRLRGEPLTVSDG 65
 DB 51 VPDTSSTSLGCPNNSNMPGFVSGSDITVALDYEAHREDLSFGKDDQVLEEDG 110
 QY 66 DMTVLSSEVSGREYNIPSVHAKV---SHGMLYEGLSREKAEELLPLGNGGAFILRE 121
 DB 111 EMMKASISLATKKEGYIPSNVAVRNLSLETENWPFKGISRKDARRHLLAGNNLGSFMRD 170
 QY 122 SOTRGSYSLVRLSRPASMDRIIRYRHCILNGMLYSPRLPPPLQALVDHYSLEAD 181
 DB 171 SETTKSSYSLVSDPDPOGSDTVYHRTKRTLDGSGGYISPSSTFSSLOELVLYKKXDG 230
 QY 182 ICLLKEPCVIGRAGPLPGK 201
 DB 231 LCKSLVPCV-----SPKPK 246
 RESULT 8
 HCK_RAT
 ID HCK_RAT STANDARD; PRT; 503 AA.
 AC P50545; Q64647;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase HCK (EC 2.7.1.112) (P56-HCK) (Hemopoietic cell
 DE kinase).
 CN HCK.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92109719; PubMed=1764064;
 RA Okano Y., Sugimoto Y., Fukuoaka M., Matsui A., Nagata K.I., Nozawa Y.;
 RT "Identification of rat cDNA encoding hck tyrosine kinase from
 RT megakaryocytes.";
 RL Biochem. Biophys. Res. Commun. 181:1137-1144(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mistar; TISSUE=Spleen;
 RA Vijaya Gouri B.S., Rama V., Kamathkar S., Swarnu G.;
 RT "Nucleotide sequence of a cDNA coding for rat hck tyrosine kinase and
 RT characterization of its gene product.";
 RL J. Biosci. 19:117-129(1994).
 CC -1- FUNCTION: MAY SERVE AS PART OF A SIGNALING PATHWAY COUPLING THE FC
 CC RECEPTOR TO THE ACTIVATION OF THE RESPIRATORY BURST. MAY ALSO
 CC CONTRIBUTE TO NEUTROPHIL MIGRATION AND MAY REGULATE THE
 CC DEGRANULATION PROCESS OF NEUTROPHILS.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Membrane-associated.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC -----
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CC EMBL; S74141; AAB20754.1; -
 CC EMBL; M83666; AAA4312.1; -
 CC EMBL; X62345; CAA44218.1; -
 CC HSSP; P08631; 1BU1.
 CC InterPro; IPR000719; Euk_pkinase.
 CC InterPro; IPR000980; SH2.
 CC InterPro; IPR001452; SH3.
 CC InterPro; IPR001245; Tyr_kinase.
 CC Pfam; PF00017; SH2; 1.
 CC Pfam; PF00018; SH3; 1.
 CC Pfam; PF00069; pkinase; 1.
 CC PRINTS; PR00401; SH2DOMAIN.
 CC PRINTS; PR00452; SH3DOMAIN.
 CC PRINTS; PR00109; TYRKINASE.
 CC ProDom; PD000001; Euk_pkinase; 1.
 CC ProDom; PD000065; SH3; 1.
 CC ProDom; PD000093; SH2; 1.
 CC SMART; SMO0326; SH3; 1.
 CC SMART; SMO0326; SH3; 1.
 CC SMART; SMO0219; TYRKC; 1.
 CC PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 CC PROSITE; PS00109; PROTEIN KINASE TYR; 1.
 CC PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 CC PROSITE; PS50001; SH2; 1.
 CC PROSITE; PS50002; SH3; 1.
 CC Transferrase; Tyrosine-protein kinase: Phosphorylation; ATP-binding;
 CC Myristate; SH2 domain; SH3 domain.
 CC FT DOMAIN 55 115 SH3.
 CC FT DOMAIN 121 218 SH2.
 CC FT DOMAIN 239 492 PROTEIN KINASE.
 CC FT NP_BIND 245 253 ATP (BY SIMILARITY).
 CC FT BINDING 267 267 ATP (BY SIMILARITY).
 CC FT ACT_SITE 358 358 BY SIMILARITY.
 CC FT LIPID 2 2 MYRISTATE (BY SIMILARITY).
 CC FT MOD_RES 388 388 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 CC FT CONFLICT 51 51 F -> V (IN REF. 2).
 CC FT CONFLICT 205 205 K -> R (IN REF. 2).
 CC FT CONFLICT 306 306 I -> T (IN REF. 2).
 CC FT SEQUENCE 503 AA; 57016 MW; A1FC1F3FE82FF73 C6C64;

Query Match 26.4%; Score 355.5; DB 1; Length 503;
 Best Local Similarity 41.4%; Pred. No. 1.1e-22; Indels 15; Gaps 4;
 Matches 84; Conservative 32; Mismatches 72;

QY 4 PSRRKSLPPSLSSVVOGQPVYMEAKRSKAT-AVALGSPAGGPAELSLRLGEPITIVS 62
 DB 33 PTSPKTLGPNINSINLPFG-----FVEGSEDTIVVALDYDEAIHREDLSFGKQGMVYLE 86
 QY 63 EDDGMMVTIVSEVSGENVNINPVAVAV-----SHGVLVEGSRREKAEELLIPGNPGAF 118
 DB 87 ESGEWMKASLATKKEGIIISNVAVKNSLETFEKFSGSKDAIRHLAPRGMLSGFM 146
 QY 119 IRESQTRGSGYSLSVRLSRPASWDRIHRIHCDNGLIYSRLTFPSGLALVDHYSSEL 178
 DB 147 IRDSEYTKGYSLSVYRDPDPQHGDTYKVKIKTLDGSGFYISPRSTFSSLDLVVHYKKG 206
 QY 179 ADDICCLKEPCVLRAGAPLPKG 201
 DB 207 KDGLCKQLSVPCV-----SPKQK 225

RESULT 9
 BLK_MOUSE STANDARD; PRT; 498 AA.
 AC P16277;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Tyrosine-protein kinase Blk (EC 2.7.1.112) (B lymphocyte kinase) (p55-
 DE Blk).
 GN Blk.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=B-cell;
 RX MEDLINE=96224819; PubMed=639560;
 RA Dymekci S.M., Niederhuber J.E., Desiderio S.V.;
 RT "Specific expression of a tyrosine kinase gene, blk, in B lymphoid
 RT cells";
 RL Science 247:332-336(1990).
 RT [2]
 RN STRUCTURE BY NMR OF SH2 DOMAIN
 RX MEDLINE=96224819; PubMed=639560;
 RA Mettler W.J., Letting B., Pryor K., Mueller L., Farmer B.T. II;
 RT "The three-dimensional solution structure of the SH2 domain from
 RT p55Blk kinase";
 RL Biochemistry 35:6201-6211(1996).
 CC -1- FUNCTION: BLK MAY FUNCTION IN A SIGNAL TRANSDUCTION PATHWAY THAT
 CC IS RESTRICTED TO B LYMPHOID CELLS.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC -1- LYSOGENE PHOSPHATE.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
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 CC or send an email to license@isb-sib.ch).

CC EMBL; M30903; AAA0453.1; -
 CC PIR; A40092; A40092.
 CC PDB; 1BLU; 12-MAR-97.
 CC PDB; 1BLK; 12-MAR-97.
 CC MCD; MG1; 88169; BLK.
 CC InterPro; IPR000719; Euk_pkinase.
 CC InterPro; IPR000980; SH2.
 CC InterPro; IPR001452; SH3.
 CC InterPro; IPR001245; Tyr_kinase.
 CC Pfam; PF00017; SH2; 1.
 CC Pfam; PF00018; SH3; 1.
 CC Pfam; PF00069; pkinase; 1.
 CC PRINTS; PR00401; SH2DOMAIN.
 CC PRINTS; PR00452; SH3DOMAIN.
 CC PRINTS; PR00109; TYRKINASE.
 CC ProDom; PD000001; Euk_pkinase; 1.
 CC ProDom; PD000065; SH3; 1.
 CC ProDom; PD000093; SH2; 1.
 CC SMART; SMO0326; SH3; 1.
 CC SMART; SMO0326; SH3; 1.
 CC SMART; SMO0219; TYRKC; 1.
 CC PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 CC PROSITE; PS00109; PROTEIN KINASE TYR; FALSE_NEG.
 CC PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 CC PROSITE; PS50001; SH2; 1.
 CC PROSITE; PS50002; SH3; 1.
 CC Tyrosine-protein kinase: Phosphorylation; Transferrase; ATP-binding;
 CC Myristate; SH2 domain; SH3 domain; 3D-structure.
 CC FT MYRISTATE 2 2 BY SIMILARITY.
 CC FT LIPID 0 0 MYRISTATE (BY SIMILARITY).
 CC FT INIT_MET 1 1 SH3.
 CC FT DOMAIN 51 111 SH2.
 CC FT DOMAIN 117 213 PROTEIN KINASE.
 CC FT DOMAIN 234 487 ATP (BY SIMILARITY).
 CC FT NP_BIND 240 248

FT BINDING 262 262 ATP (BY SIMILARITY).
 FT ACT SITE 353 353 BY SIMILARITY.
 FT MOD RES 382 382 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 SQ SEQUENCE 498 AA; 56513 MW; B849D78079FD577 CRC64;

Query Match 25.7%; Score 345.5; DB 1; Length 498;
 Best Local Similarity 40.5%; Pred. No. 7.6e-22;
 Matches 75; Conservative 29; Mismatches 64; Indels 17; Gaps 3;

QY 11 PPSPLSSSSVQGGPVTMEERKATNAVALGSPAGAPALSLRGEPLTVSDGDMTV 70
 DB 43 PSPN-----QDDDEERFVALDYAAVNDRLQVLGSEKLQVLRSTGDMWMA 90
 QY 71 LSEVSGREYNIPIPSVHAKVS---HGWLVEGLSREKABELLLPFGCAFLIREQTRR 126
 DB 91 RSLVTGREGYVPSNFVAPEVLEVKWFPRITSRKDAERQLALPMNAAGSFLIRESENK 150
 QY 127 GSYSLVRLSRPASMDRIIRHYRHCILNGLYSPRLTPEPSQLVDHYSGLADICLL 186
 DB 151 GAFSLSVK-DITTOGEVWVKHKISLNDGTYISPRITFPTLLQALVGHYSKKGDLQGL 209
 QY 187 KEPCV 191
 DB 210 TLPCV 214

RESULT 10
 LCK_HUMAN

ID LCK_HUMAN STANDARD; PRT; 508 AA.
 AC P06239; F07100; Q9NYTB; Q96DW4; Q13152; Q12850;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK)
 GN LCK (T cell-specific protein-tyrosine kinase).
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RA Perlmutter R.M., Marth J.D., Lewis D.B., Peet R., Ziegler S.F.,
 RA Wilson C.B.,
 RT "Structure and expression of lck transcripts in human lymphoid
 RT cells.";
 RL J. Cell. Biochem. 38:117-126(1988).
 RP SEQUENCE FROM N.A.
 RA MEDLINE=87133831; PubMed=3493153;
 RA Koga Y., Caccia N., Toyonaga B., Spolski R., Yanagi Y., Yoshikai Y.,
 RA Mak T.W.,
 RT "A human T cell-specific cDNA clone (YT16) encodes a protein with
 RT extensive homology to a family of protein-tyrosine kinases.";
 RL Eur. J. Immunol. 16:1643-1646(1986).
 RP SEQUENCE FROM N.A.
 RA MEDLINE=90108697; PubMed=2558056;
 RA Rorer E., van Huynh T., de Souza S.L., Lang M.C., Fischer S.,
 RA Benarous R.,
 RT "Structure of the human lck gene: differences in genomic organisation
 RT within src-related genes affect only N-terminal exons.";
 RL Gene 84:105-113(1989).
 RP SEQUENCE FROM N.A., VARIANTS L-27; POKP-231 INS; V-352, L-446, AND
 RP PHOSPHORYLATION OF TYR-393 AND TYR-504.
 RC TISSUE=Leukemia;
 RX MEDLINE=9418714; PubMed=8139546;
 RA Wright D.D., Sefton B.M., Kamps M.P.,
 RT "Oncogenic activation of the lck protein accompanies translocation of
 RT the lck gene in the human HSB2 T-cell leukemia.";
 RL Mol. Cell. Biol. 14:2429-2437(1994).

RN [5]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=Leukemic T-cell;
 RX MEDLINE=96085119; PubMed=7495859;
 RA Vogel L.B., Arthur R., Fujita D.J.,
 RT "An aberrant lck mRNA in two human T-cell lines.";
 RL Biochim. Biophys. Acta 1264:168-172(1995).
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph;
 RA Strausberg R.,
 RL Submitted (Aug-2001) to the EMBL/Genbank/DBJ databases.
 RP SEQUENCE OF 13-508 FROM N.A.
 RC TISSUE=Peripheral blood lymphocytes;
 RX MEDLINE=20462621; PubMed=11009097;
 RA Boncristiano W., Majolini M.B., D'Elia M.M., Pacini S., Valensin S.,
 RA Ulivieri C., Amedei A., Falini B., Del Prete G., Telford J.L.,
 RA Baldari C.T.,
 RT "Defective recruitment and activation of ZAP-70 in common variable
 RT immunodeficiency patients with T cell defects.";
 RL Eur. J. Immunol. 30:2632-2638(2000).
 RP SEQUENCE OF 367-508 FROM N.A.
 RX MEDLINE=88217332; PubMed=2835736;
 RA Velliette A., Foss F.M., Sausville E.A., Bolen J.B., Rosen N.,
 RT "Expression of the lck tyrosine kinase gene in human colon carcinoma
 RT and other non-lymphoid human tumor cell lines.";
 RL Oncogene Res. 1:357-374(1987).
 RP SEQUENCE OF 374-508 FROM N.A.
 RX MEDLINE=87000726; PubMed=3489486;
 RA Trevillyan J.M., Lin Y., Chen S.J., Phillips C.A., Canna C.,
 RA Lima T.J.,
 RT "Human T lymphocytes express a protein-tyrosine kinase homologous to
 RT p56LCK.";
 RL Blochim. Biophys. Acta 888:286-295(1986).
 RP SEQUENCE OF 1-34 FROM N.A.
 RX MEDLINE=89096891; PubMed=2850479;
 RA Garvin A.M., Pavar S., Marth J.D., Perlmutter R.M.,
 RT "Structure of the murine lck gene and its rearrangement in a murine
 RT lymphoma cell line.";
 RL Mol. Cell. Biol. 8:3058-3064(1988).
 RP SEQUENCE OF 1-34 FROM N.A.
 RX MEDLINE=89313764; PubMed=2787474;
 RA Takadera T., Leung S., Gernone A., Koga Y., Takihara Y.,
 RA Miyamoto N.G., Mak T.W.,
 RT "Structure of the two promoters of the human lck gene: differential
 RT accumulation of two classes of lck transcripts in T cells.";
 RL Mol. Cell. Biol. 9:2173-2180(1989).
 RP MASS SPECTROMETRY.
 RC TISSUE=Breast cancer;
 RX MEDLINE=21829512; PubMed=11840567;
 RA Harris R.A., Yang A., Stein R.C., Lucy K., Brusten L., Herath A.,
 RA Paten R., Waterfield M.D., O'Hare W.J., Neville M.A., Page M.J.,
 RA Zvelebil M.J.,
 RT "Cluster analysis of an extensive human breast cancer cell line
 RT protein expression map database.";
 RL Proteomics 2:212-223(2002).
 RP INTERACTION WITH PI3K.
 RX MEDLINE=94067101; PubMed=7504174;
 RA Vogel L.B., Fujita D.J.,
 RT "The SH3 domain of p56Lck is involved in binding to
 RT phosphatidylinositol 3'-kinase from T lymphocytes.";
 RL Mol. Cell. Biol. 13:7408-7417(1993).
 RP INTERACTION WITH KHDRBS1.
 RX MEDLINE=9515308; PubMed=7852312;
 RA Vogel L.B., Fujita D.J.,

[illegible]

RT "Avian reovirus mRNAs are nonfunctional in infected mouse cells:
translational basis for virus host-range restriction.";
Proc. Natl. Acad. Sci. U.S.A. 85:4257-4261(1988).
[6]
RX MUTAGENESIS.
MEDLINE=93059694; PubMed=1279202;
RA Hurley T.R., Amrein K.E., Sefton B.M.;
RT "Creation and characterization of temperature-sensitive mutants of
the tick tyrosine protein kinase.";
J. Virol. 66:7406-7413(1992).
RN [7]
RX MUTAGENESIS OF LYS-272.
MEDLINE=91163633; PubMed=1706070;
RA Abraham N., Miceli M.C., Parnas J.C., Velliste A.;
RT "Enhancement of T-cell responsiveness by the lymphocyte-specific
tyrosine protein kinase p56lck.";
Nature 350:62-66(1991).
RN [8]
RX MUTAGENESIS OF TYR-504.
MEDLINE=91219495; PubMed=1708890;
RA Abraham K.M., Levin S.D., Marsh J.D., Forbush K.A., Perlmuter R.M.;
RT "Thymic tumorigenesis induced by overexpression of p56lck.";
Proc. Natl. Acad. Sci. U.S.A. 88:3977-3981(1991).
RN [9]
RX MUTAGENESIS.
MEDLINE=93133805; PubMed=8421674;
RA Carrera A.C., Alexandrov K., Roberts T.M.;
RT "The conserved lysine in the catalytic domain of protein kinases is
actively involved in the phosphotransfer reaction and not required
for anchoring ATP.";
Proc. Natl. Acad. Sci. U.S.A. 90:442-446(1993).
RN [10]
RX PALMITOYLATION.
MEDLINE=94019312; PubMed=8413237;
RA Shenoy-Scaria A.M., Timson L.K., Kwong J., Shaw A.S., Lublin D.M.;
RT Palmitoylation of an amino-terminal cysteine motif of protein
tyrosine kinases p56lck and p59fyn mediates interaction with
glycosyl-phosphatidylinositol-anchored proteins.";
Mol. Cell. Biol. 13:6385-6392(1993).
RN [11]
RX PALMITOYLATION.
MEDLINE=95071286; PubMed=7980442;
RA Koegl M., Ziaekine P., Ley S.C., Coutneide S.A., Magee A.I.;
RT "Palmitoylation of multiple Src-family kinases at a homologous N-
terminal motif.";
Biochem. J. 303:749-753(1994).
CC -1- FUNCTION: MAY PARTICIPATE IN ANTIGEN-INDUCED T-CELL ACTIVATION.
ITS EARLY EXPRESSION IS ESSENTIAL FOR EARLY T-LYMPHOCYTE
DEVELOPMENT.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
tyrosine phosphate
CC -1- SUBCELLULAR LOCATION: BOUND TO THE CYTOPLASMIC DOMAIN OF EITHER
CD4 OR CD8.
CC -1- TISSUE SPECIFICITY: PRESENT AT A LOW LEVEL IN MOST T CELLS, AND
AT AN ELEVATED LEVEL IN LSTRA AND THY 19 (T-CELL LYMPHOMA) CELLS.
CC -1- DEVELOPMENTAL STAGE: LEVELS REMAIN RELATIVELY CONSTANT THROUGHOUT
T-CELL ONTOGENY.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CC -----
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CC -----
DR EMBL; X03533; CA27234.1; -;
DR EMBL; M2056; AAB59674.1; -;
DR EMBL; X03533; CA27235.1; ALT_SEQ.

DR EMBL; X03533; CA27236.1; ALT_SEQ.
DR EMBL; M2151; AAA39422.1; ALT_SEQ.
DR EMBL; M18098; AAA39421.1; -;
DR PIR; A23639; A23639.
DR HSP; P06219; 11CK.
DR MGD; MGT196756; 1CK.
DR InterPro; IPR007179; Euk_pkinase.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR01452; SH3.
DR InterPro; IPR01245; Tyr_pkinase.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PRO0452; SH2DOMAIN.
DR PRINTS; PRO0452; SH3DOMAIN.
DR PRINTS; PRO0109; TYRKINASE.
DR ProDom; PD000066; SH3; 1.
DR ProDom; PD000093; SH2; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50002; SH3; 1.
KW Proto-oncogene; Tyrosine-protein kinase; Phosphorylation; Transferase;
KW ATP-binding; Myristate; SH2 domain; SH3 domain; Palmitate;
KW Lipoprotein.
FT INIT MET 0 0 PROBABLE.
FT LIPID 1 1 MYRISTATE (BY SIMILARITY).
FT LIPID 2 2 PALMITATE.
FT LIPID 4 4 PALMITATE.
FT DOMAIN 60 120 SH3.
FT DOMAIN 126 223 SH2.
FT DOMAIN 244 497 PROTEIN KINASE.
FT NP BIND 250 258 APP (BY SIMILARITY).
FT BINDING 272 272 APP (BY SIMILARITY).
FT ACT SITE 363 363 BY SIMILARITY.
FT MOD_RES 363 363 PHOSPHORYLATION (NEGATIVE REGULATION) (BY
MOD_RES 504 504 SIMILARITY).
FT MUTAGEN 268 268 K->N: REDUCED ACTIVITY.
FT MUTAGEN 269 269 V->L: REDUCED ACTIVITY.
FT MUTAGEN 270 270 A->S: REDUCED ACTIVITY.
FT MUTAGEN 271 271 V->R: REDUCED ACTIVITY.
FT MUTAGEN 272 272 K->R: LOSS OF ACTIVITY.
FT MUTAGEN 273 273 S->N: REDUCED ACTIVITY.
FT MUTAGEN 274 274 L->M: REDUCED ACTIVITY.
FT MUTAGEN 275 275 K->V: REDUCED ACTIVITY.
FT MUTAGEN 504 504 Y->F: CAUSES THYMIC TUMORS.
FT CONFLICT 282 283 VP->S DA (IN REF. 2).
SQ SEQUENCE 508 AA; 57821 MW; E92562498CAF6878 CRC64;
Query Match 25.4%; Score 342.5; DB 1; Length 508;
Best Local Similarity 39.6%; Pred. No. 1,4e-21;
Matches 78; Conservative 28; Mismatches 84; Indels 7; Gaps 2;
QY 2 SLPSRRKSLPSPLSSSSVVOGQGPVTMEARSKATAVALGFPAGPAEISRLGEPTIV 61
DB 34 SLPIRNGSEVRDPL---VTEGSLPPASPLQDNVIALHSYERSHDGDGKEKGEQRL 90
QY 62 SEGDWWTWLVSGVREYVNPSTHYAKYS---HGWLYESLSREKAEELLRLGNPGAF 117
DB 91 EGGEWKKAKSLITTGCGFLPFPYFAKANSLEPPPEFKSLSKONEQLAPENTHGSF 150
QY 118 LIRESGTRRGYSVSLSPASWDRIRHYIHCLDGMWLYSPRLPPSLQALVDHYSP 177
DB 151 LIRESSTAGSRPSLVDPDONGEVGVHYKIRMLDNGGYISPRITPPGLHDLVRYTN 210
QY 178 LADDICLLKEPCVLR 194

Db 211 ASDGLCTLSRPCOTOK 227

RESULT 12

LCK_CHICK STANDARD; PRT; 507 AA.

AC P42683;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Proco-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (Protein-tyrosine kinase C-TKL).

GN LCK.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

OC NCBI_TaxID=9031;

OX [1]

RP SEQUENCE OF 1-88 FROM N.A.

RX MEDLINE=8097370; PubMed=3321053;

RA Chow L., Ratcliffe M., Velliet A.

RT "Lck is the avian homolog of the mammalian lck tyrosine protein kinase gene."

RL Mol. Cell. Biol. 12:1226-1233(1992).

RN [2]

RP SEQUENCE OF 46-507 FROM N.A.

RX MEDLINE=8097370; PubMed=3321053;

RA Strehardt K., Mullins J.I., Bruck C., Ruebsamen-Waigmann H.; "Additional member of the protein-tyrosine kinase family: the src- and lck-related protooncogene c-lck."

RL Proc. Natl. Acad. Sci. U.S.A. 84:8778-8782(1987).

CC -1- FUNCTION: MAY PARTICIPATE IN ANTIGEN-INDUCED T-CELL ACTIVATION.

CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.

CC -1- SUBCELLULAR LOCATION: BOUND TO THE CYTOPLASMIC DOMAIN OF EITHER CD4 OR CD8.

CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC SUBFAMILY.

CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.

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CC -----

DR EMBL; M85043; AAA49003.1; -

DR EMBL; J03579; AAA49081.1; ALT_INIT.

DR HSPB; P06239; 3LCK.

DR InterPro: IPR000719; Euk_pkinase.

DR InterPro: IPR000980; SH2.

DR InterPro: IPR001452; SH3.

DR InterPro: IPR001245; Tyr_pkinase.

DR Pfam; PF00017; SH2; 1.

DR Pfam; PF00018; SH3; 1.

DR Pfam; PF00069; pkinase; 1.

DR PRINTS; PR00401; SH2DOMAIN.

DR PRINTS; PR00452; SH2DOMAIN.

DR PRINTS; PR00109; TYRKINASE.

DR ProDom; PD000001; Euk_pkinase; 1.

DR ProDom; PD000066; SH3; 1.

DR ProDom; PD000093; SH2; 1.

DR SMART; SM00252; SH2; 1.

DR SMART; SM00326; SH3; 1.

DR SMART; SM00219; Tyrc; 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.

DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.

DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00011; SH2; 1.

DR PROSITE; PS00022; SH3; 1.

KW Proco-oncogene; Tyrosine-protein kinase; Phosphorylation; Transferase;

KW ATP-binding; Myristate; SH2 domain; SH3 domain; Palmitate;

KW Lipoprotein.

FT INIT MET 0 0 PROBABLE.

FT LIPID 1 1 MYRISTATE (BY SIMILARITY).

FT LIPID 2 2 PALMITATE (BY SIMILARITY).

FT LIPID 4 4 PALMITATE (BY SIMILARITY).

FT LIPID 59 119 SH3.

FT DOMAIN 125 222 SH2.

FT DOMAIN 243 496 PROTEIN KINASE.

FT NP_BIND 249 257 ATP (BY SIMILARITY).

FT BINDING 271 271 ATP (BY SIMILARITY).

FT ACT_SITE 362 362 BY SIMILARITY.

FT MOD_RES 392 392 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

FT MOD_RES 503 503 PHOSPHORYLATION (NEGATIVE REGULATION) (BY SIMILARITY).

FT SQ SEQUENCE 507 AA; 58008 MW; BC3C4FA89186170 CRC64;

Query Match 25.0%; Score 337; DB 1; Length 507;

Best Local Similarity 43.8%; Pred. No. 4.1e-21;

Matches 71; Conservative 27; Mismatches 60; Indels 4; Gaps 1;

Qy 37 VALGSPAGAPAEPLSLRGEPLTIVSEDPGDMWTIVSEVSGREYVPEVAVAKV-----HG 92

Db 65 VALVDYEPHTDGDGLKQCEKLRVLEBSGEMWRAQSITTCGEGILPFIAMWNSLEDEP 124

Qy 93 WLVEGLSREKAEELLLPNCPCAFILRESQTRSGSYSLVRLSPASWDRIHRIHCL 152

Db 125 WFKVLGRKAEARLLASGNTGHSFLLIRESETSKSYSLVRPDQNOGTYVHYKINM 184

Qy 153 DNGCWLYSPRLTPPSLQALVDHYSELADICCLKEPCVLR 194

Db 185 DNGGYISFPRYTSLSLHELVYSSSDGLCTRLGPRCTOK 226

RESULT 13

ID YES_XENIA STANDARD; PRT; 537 AA.

AC P10936;

DT 01-JUL-1989 (Rel. 11, Created)

DT 01-JUL-1989 (Rel. 11, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Proco-oncogene tyrosine-protein kinase YES (EC 2.7.1.112) (P61-YES) (C-YES).

GN YES.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae; Xenopus.

OC NCBI_TaxID=8355;

OX [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=89296347; PubMed=2472952;

RA Steele R.E., Irwin M.Y., Knudsen C.L., Collett J.W., Pero J.B.; "The yes proto-oncogene is present in amphibians and contributes to the maternal RNA pool in the oocyte."

RL Oncogene Res. 4:223-233(1989).

CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.

CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC SUBFAMILY.

CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.

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CC -----

FT DOMAIN 89 150 SH3.
 FT DOMAIN 156 253 SH2.
 FT DOMAIN 275 528 PROTEIN KINASE.
 FT NP_BIND 281 289 ATP (BY SIMILARITY).
 FT BINDING 303 303 ATP (BY SIMILARITY).
 FT ACT_SITE 394 394 BY SIMILARITY.
 FT MOD_RES 424 424 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT CONFLICT 67 71 TPFG -> IHPK (IN REF. 3).
 FT CONFLICT 82 82 P -> Q (IN REF. 3).
 SQ SEQUENCE 541 AA; BEA849CCTD1755AF CRC64;
 Query Match 23.84; Score 321; DB 1; Length 541;
 Best Local Similarity 31.84; Pred. No. 1e-19;
 Matches 92; Conservative 43; Mismatches 104; Indels 50; Gaps 9;

QY 1 GSLSRRKSLPSPSLSSVGGQGPVTMEAKSKATVALGSPFAGPAELSLRLEPLTI 60
 DB 70 GGASSSFSAVPSPPSTLT--GGVTV-----FVALDYEARFTDLSFKGGERFOI 118
 QY 61 VSB-DGDMWTVLSEVSGREYVPSVAVAKV-----SHQWYEGREKAEELLPLGNRG 115
 DB 119 INTEGDWWEARSATGKTGYISNVYAPADSIQAEWYFGKGRKADARLLPNQNG 178
 QY 116 AFLIRSSQTRGSGYSLVRLSPASDRIR-----HRIHCDNGMLYISPLTFPSLQ 170
 DB 179 IFLVRSSETTKGAYSLIR-----DWDEVGDNVYKIRKLDNGGYITTRAFESLQK 233
 QY 171 LVHYSELADICCLKEPC-----VLQRAPLPGKDIPLPTVOR-----211
 DB 234 LVHYREHADGCHLTTCVPTVKPTQGLADAMEIPRESLLEVKAGQCFGVWMT 233
 QY 212 ----TPLNKELDSSLLFSEANGESLLSEGLRSL-SFYISLNDKAN 255
 DB 294 WNGTTVAIKTLKPGTWMPEAFLOEQIMKKLRHKLVPLAVVSEPT 342

RESULT 15
 FYN_HUMAN STANDARD; PRT; 536 AA.
 AC P06241;
 DT 01-JAN-1988 (rel. 06, Created)
 DT 01-FEB-1994 (rel. 28, Last sequence update)
 DT 15-JUN-2002 (rel. 41, Last annotation update)
 DE Proto-oncogene tyrosine-protein kinase FYN (EC 2.7.1.112) (P59-FYN)
 DE (SYN) (SLK).
 GN FYN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 OX [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=6287278; PubMed=3526330;
 RA Senba K., Nishizawa M., Miyajima N., Yoshida M.C., Sukegawa J.,
 RA Yamashita Y., Sasaki M., Yamamoto T., Toyoshima K.:
 RT "Yas-related protooncogene, syn. belongs to the protein-tyrosine
 RT kinase family.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:5459-5463(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87089775; PubMed=3099169;
 RA Kawakami T., Pennington C.Y., Robbins K.C.:
 RT "Isolation and oncogenic potential of a novel human src-like gene.";
 RL Mol. Cell. Biol. 6:4195-4201(1986).
 RN [3]
 RP MYRISTOYLATION, AND PHOSPHORYLATION OF TYR-530.
 RX MEDLINE=91016431; PubMed=1699196;
 RA Peters D.J., McGrew B.R., Perron D.C., Liptrak L.M., Laudano A.P.:
 RT "In vivo phosphorylation and membrane association of the Fyn proto-
 RT oncogene product in IM-9 human lymphoblasts.";
 RL Oncogene 5:1313-1319(1990).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF SH3 DOMAIN.

RX MEDLINE=93327750; PubMed=7687536;
 RA Noble M.E.M., Musacchio A., Saraste M., Courtneidge S.A.,
 RA Wierenga R.K.:
 RT "Crystal structure of the SH3 domain in human Fyn: comparison of the
 RT three-dimensional structures of SH3 domains in tyrosine kinases and
 RT spectrin.";
 RL EMBO J. 12:2617-2624(1993).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 80-141.
 RX MEDLINE=95393198; PubMed=764083;
 RA Musacchio A., Saraste M., Williams M.:
 RT "High-resolution crystal structures of tyrosine kinase SH3 domains
 RT complexed with proline-rich peptides.";
 RL Nat. Struct. Biol. 1:546-551(1994).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 84-140 IN COMPLEX WITH NEF.
 RX MEDLINE=96279837; PubMed=8681387;
 RA Lee C.H., Saksela K., Mirza U.A., Chait B.T., Kuriyan J.:
 RT "Crystal structure of the conserved core of HIV-1 Nef complexed with
 RT a Src family SH3 domain.";
 RL Cell 85:931-942(1996).
 RN [7]
 RP STRUCTURE BY NMR OF SH3 DOMAIN.
 RX MEDLINE=96399716; PubMed=880554;
 RA Morton C.V., Pugh D.V.R., Brown E.L.J., Kahmann J.D., Renzoni D.A.C.,
 RA Campbell I.D.:
 RT "Solution structure and peptide binding of the SH3 domain from human
 RT Fyn.";
 RL Structure 4:705-714(1996).
 RN [8]
 RP STRUCTURE BY NMR.
 RX MEDLINE=97121261; PubMed=8961927;
 RA Renzoni D.A., Pugh D.V., Siligardi G., Dae P., Morton C.J., Rossi C.,
 RA Waterfield M.D., Campbell I.D., Ladbury J.E.:
 RT "Structural and thermodynamic characterization of the interaction of
 RT the SH3 domain from Fyn with the proline-rich binding site on the p85
 RT subunit of p13-kinase.";
 RL Biochemistry 35:15646-15653(1996).
 RN [9]
 RP STRUCTURE BY NMR OF SH2 DOMAIN.
 RX MEDLINE=98035454; PubMed=9351806;
 RA Mulhern T.D., Shaw G.V., Morton C.J., Day A.J., Campbell I.D.:
 RT "The SH2 domain from the tyrosine kinase Fyn in complex with a
 RT phosphotyrosyl peptide reveals insights into domain stability and
 RT binding specificity.";
 RL Structure 5:1313-1323(1997).
 RN [10]
 RP BINDING OF SH3 DOMAIN TO PI 3-KINASE.
 RX MEDLINE=93348274; PubMed=8394019;
 RA Prasad K.V., Janssen O., Kapeller R., Raab M., Cantley L.C.,
 RA Rudd C.E.:
 RT "Src-homology 3 domain of protein kinase p59fyn mediates binding to
 RT phosphatidylinositol 3-kinase in T cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:7366-7370(1993).
 CC - FUNCTION: IMPLICATED IN THE CONTROL OF CELL GROWTH.
 CC - CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC - SUBUNIT: ASSOCIATES THROUGH ITS SH3 DOMAIN, TO THE P85 SUBUNIT OF
 CC PHOSPHATIDYLINOSITOL 3-KINASE. INTERACTS WITH THE FYN-BINDING
 CC PROTEIN (FYN).
 CC - SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUBFAMILY.
 CC - SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC - SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC
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QY 9 SLPSLSVVGGPVTMEERSKATA-----VALGSFPAGPAELSLRL 54

Search completed: March 24, 2003, 15:46:09
Job time : 15.0303 secs

